

CD105PCT.ST25.txt  
SEQUENCE LISTING

<110> CropDesign N.V.

<120> Plants having modified growth characteristics and method for making the same

<130> CD-105-PCT

<150> US 60/528,113

<151> 2003-12-09

<150> EP 03104280.7

<151> 2003-11-19

<160> 18

<170> PatentIn version 3.3

<210> 1

<211> 1428

<212> DNA

<213> Nicotiana tabacum

<220>

<221> misc\_feature

<223> seedy1 coding sequence (CDS0689)

<400> 1

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ctgaaacccc	tttcggttag	gccatcagat	tcctttgaat	ctgatttgtc	aagtaaggaa	180
aatcaaactc	ctttatttga	gaattcatct	gttaatctct	catctccgtt	acccataaag	240
ccacttaacc	ctaattgggc	tctggaaaat	tcaagactca	agccgaacaa	gccaattcc	300
aaacagagtc	ttgatgagat	ggcggctaga	aagagcggaa	agggaaatga	tttccgtgat	360
gagaagaaaa	tagacgagga	aattgaagaa	attcagatgg	agattagtag	gttgagttca	420
agatttagagg	ctttgagaat	tgaaaaggct	gagaaaactg	ttgctaagac	tgttgaaaag	480
cgaggaaggg	ttgtggcagc	aaagtttatg	gagccaaaac	aaagtgttat	taagattgaa	540
gagcgtatat	caatgagtgc	aagaacaaaag	gtggagcaga	gaaggggtct	tagtttagga	600
ccatctgaga	tttttactgg	aacgcggcgg	cgagggttga	gtatggggcc	atcagatatt	660
ctagcaggga	caacaaaggc	acggcaattg	ggaaagcaag	agatgattat	tactcctatt	720
cagccaatac	aaaacaggcg	aaagtcgtgt	ttttggaagc	ttcaagagat	tgaagaagag	780
ggaaaaagtt	caagccttag	tcctaaatca	agaaaaactg	ctgcaagaac	aatggttaca	840
acaaggcagg	cagttactac	aattgcatca	aagaagaatt	tgaaaaaaga	tgatggactt	900
ttgagttcag	ttcagccaaa	gaagttgttt	aaagatctcg	aaaagtctgc	tgctgctaatt	960
aagaagcccc	agaggccggg	gagggttgtg	gctagtaggt	ataatcagag	tacaattcag	1020
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gataagaaac	ggtcgttatc	tgtagggaaa	acgcgtgtgt	ctcaaactga	gagcaagaat	1140
ttgggtactg	aaagttaggt	gaaaaagaga	tgggaaattc	ctagtgagat	tgtagttcat	1200
ggaaacacag	agagtgagaa	atctccacta	agcattattg	tgaagcctga	tttgcttccg	1260
cgaattagga	ttgctcgggt	tgtgaatgag	actcttaggg	attctggacc	tgctaaaaga	1320
atgatagagt	tgataggcaa	gaaatcgttt	ttcagtagtg	atgaagataa	ggagccacct	1380
gtctgtcaag	ttttaagttt	tgcagaggaa	gatgctgaag	aggaataa		1428

<210> 2

<211> 475

<212> PRT

<213> Nicotiana tabacum

CD105PCT.ST25.txt

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;223&gt; seedy1 protein (CDS0689)

&lt;400&gt; 2

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Met Ser Val Leu Gln Tyr Pro Glu Gly Ile Asp Pro Ala Asp Val Gln
1          5          10          15

Ile Trp Asn Asn Ala Ala Phe Asp Asn Gly Asp Ser Glu Asp Leu Ser
          20          25          30

Ser Leu Lys Arg Ser Trp Ser Pro Leu Lys Pro Leu Ser Val Arg Pro
          35          40          45

Ser Asp Ser Phe Glu Ser Asp Leu Ser Ser Lys Glu Asn Gln Thr Pro
          50          55          60

Leu Phe Glu Asn Ser Ser Val Asn Leu Ser Ser Pro Leu Pro Ile Lys
65          70          75          80

Pro Leu Asn Pro Asn Gly Ala Leu Glu Asn Ser Arg Leu Lys Pro Asn
          85          90          95

Lys Pro Asn Ser Lys Gln Ser Leu Asp Glu Met Ala Ala Arg Lys Ser
          100          105          110

Gly Lys Gly Asn Asp Phe Arg Asp Glu Lys Lys Ile Asp Glu Glu Ile
          115          120          125

Glu Glu Ile Gln Met Glu Ile Ser Arg Leu Ser Ser Arg Leu Glu Ala
          130          135          140

Leu Arg Ile Glu Lys Ala Glu Lys Thr Val Ala Lys Thr Val Glu Lys
145          150          155          160

Arg Gly Arg Val Val Ala Ala Lys Phe Met Glu Pro Lys Gln Ser Val
          165          170          175

Ile Lys Ile Glu Glu Arg Ile Ser Met Ser Ala Arg Thr Lys Val Glu
          180          185          190

Gln Arg Arg Gly Leu Ser Leu Gly Pro Ser Glu Ile Phe Thr Gly Thr
          195          200          205

Arg Arg Arg Gly Leu Ser Met Gly Pro Ser Asp Ile Leu Ala Gly Thr
          210          215          220

Thr Lys Ala Arg Gln Leu Gly Lys Gln Glu Met Ile Ile Thr Pro Ile
225          230          235          240

Gln Pro Ile Gln Asn Arg Arg Lys Ser Cys Phe Trp Lys Leu Gln Glu
          245          250          255

Ile Glu Glu Glu Gly Lys Ser Ser Ser Leu Ser Pro Lys Ser Arg Lys
          260          265          270

Thr Ala Ala Arg Thr Met Val Thr Thr Arg Gln Ala Val Thr Thr Ile
          275          280          285

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## CD105PCT.ST25.txt

Ala Ser Lys Lys Asn Leu Lys Lys Asp Asp Gly Leu Leu Ser Ser Val  
 290 295 300

Gln Pro Lys Lys Leu Phe Lys Asp Leu Glu Lys Ser Ala Ala Ala Asn  
 305 310 315 320

Lys Lys Pro Gln Arg Pro Gly Arg Val Val Ala Ser Arg Tyr Asn Gln  
 325 330 335

Ser Thr Ile Gln Ser Ser Val Val Arg Lys Arg Ser Leu Pro Glu Asn  
 340 345 350

Asp Lys Asp Glu Ser Lys Arg Asn Asp Lys Lys Arg Ser Leu Ser Val  
 355 360 365

Gly Lys Thr Arg Val Ser Gln Thr Glu Ser Lys Asn Leu Gly Thr Glu  
 370 375 380

Ser Arg Val Lys Lys Arg Trp Glu Ile Pro Ser Glu Ile Val Val His  
 385 390 395 400

Gly Asn Thr Glu Ser Glu Lys Ser Pro Leu Ser Ile Ile Val Lys Pro  
 405 410 415

Asp Leu Leu Pro Arg Ile Arg Ile Ala Arg Cys Val Asn Glu Thr Leu  
 420 425 430

Arg Asp Ser Gly Pro Ala Lys Arg Met Ile Glu Leu Ile Gly Lys Lys  
 435 440 445

Ser Phe Phe Ser Ser Asp Glu Asp Lys Glu Pro Pro Val Cys Gln Val  
 450 455 460

Leu Ser Phe Ala Glu Glu Asp Ala Glu Glu Glu  
 465 470 475

<210> 3  
 <211> 1336  
 <212> DNA  
 <213> Oryza sativa

<220>  
 <221> misc\_feature  
 <223> secdyl coding sequence

<400> 3  
 atggaggagg accgctcat cccgctggtc cacgtctgga acaacgccgc cttcgacgac 60  
 tcctcgtgtt ccagatcggc ttggctcccc caaagccccg ccgtcgcggc cgtccgcaag 120  
 ggcgacaagg agaatcaccg ccccgagggt gttgatgtcg ccgccggcta cgacgtcgag 180  
 gccgagatcg gccacatcga ggcggagatc ctgcgcctct cgtcccggct ccaccatctc 240  
 cgcgtctcca agcagccgga gcccaaccgc gacgacgtc cgatggggga gatggtcgag 300  
 aaggtgaggc cccggccgag gggcctcagc ctccggcccc tggatgtgat ctccatcgtc 360  
 aatcgtgaga agcatccgct gcgcaccaag cagcctccgg cgacgcgggg cagggggctc 420  
 agcctcgggc ccatggagat cgccgcggcg aaccctaggg tgcccgcggc ggcgcagcat 480  
 cagcaacagc aacgcgctgg cacggcgagg atcctgaagc caatcaagga gcctccgggtg 540  
 cagcgtcgca gggcgctcag cctcggggccg ttggagatcc accacggcgt cggcagcaag 600  
 gcaccagcgg cggcgcgagc caagcggttc accaccaagc tcaacgccat tcgagaagaa 660  
 acccgaccct ccaagcaatt cgccgtcccc gccaaagccat ggccgtcgag caatacaagg 720  
 cagacactgg actcgaggca aggaacagca gcaagtcgag cgaaggcgag gagcccagag 780

## CD105PCT.ST25.txt

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cccaggccca ggaggcaatc caatggcaag gctactgaca caaggggagg caacaaggtg      840
gtggatgagc tcaagcccaa aggtgctgctg tcaagtcaga gcggcagcgc cgccgccgcc      900
gccactgcc aagagatggc ggggagctcc aagatgaggg tcatcccag cgcctacagc      960
ctcactcctg gcgcttcctt tggaagcagt ggagcacagg agaggcgacg caagcagtct     1020
ctcccaggat catcagggga tgcgaaccag aatgaggaaa tcagagcgaa ggtcatcgag     1080
ccttccaatg atccactctc tcctcaaacg atctccaagg ttgctgaaat gctcccaaag     1140
atcaggacca tgccgcctcc tgacgagagc cctcgcgatt ccggatgcgc caagcggggt     1200
gccgaattgg tcgggaagcg ctcgttcttc acggtgcag ccgaggacgg gcgggcgctc     1260
gacgtcgaag cacccgaggc ggtcgcagaa gcttgagatg aaccaccatg gtttgatccg     1320
ttccttccat cagctc                                     1336

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<210> 4  
 <211> 431  
 <212> PRT  
 <213> Oryza sativa

<220>  
 <221> MISC\_FEATURE  
 <223> seedy1 protein

<400> 4  
 Met Glu Glu Asp Pro Leu Ile Pro Leu Val His Val Trp Asn Asn Ala  
 1 5 10 15  
 Ala Phe Asp Asp Ser Ser Cys Ser Arg Ser Ala Trp Leu Pro Gln Ser  
 20 25 30  
 Pro Ala Val Ala Ala Val Arg Lys Gly Asp Lys Glu Asn His Arg Pro  
 35 40 45  
 Glu Val Val Asp Val Ala Ala Gly Tyr Asp Val Glu Ala Glu Ile Gly  
 50 55 60  
 His Ile Glu Ala Glu Ile Leu Arg Leu Ser Ser Arg Leu His His Leu  
 65 70 75 80  
 Arg Val Ser Lys Gln Pro Glu Pro Asn Arg Asp Asp Ala Pro Met Gly  
 85 90 95  
 Glu Met Val Ala Lys Val Arg Pro Arg Pro Arg Gly Leu Ser Leu Gly  
 100 105 110  
 Pro Leu Asp Val Ile Ser Ile Val Asn Arg Glu Lys His Pro Leu Arg  
 115 120 125  
 Thr Lys Gln Pro Pro Ala Thr Arg Gly Arg Gly Leu Ser Leu Gly Pro  
 130 135 140  
 Met Glu Ile Ala Ala Ala Asn Pro Arg Val Pro Ala Ala Ala Gln His  
 145 150 155 160  
 Gln Gln Gln Gln Arg Ala Gly Thr Ala Arg Ile Leu Lys Pro Ile Lys  
 165 170 175  
 Glu Pro Pro Val Gln Arg Arg Arg Gly Val Ser Leu Gly Pro Leu Glu  
 180 185 190  
 Ile His His Gly Val Gly Ser Lys Ala Pro Ala Ala Ala Arg Ala Lys  
 195 200 205

## CD105PCT.ST25.txt

Pro Phe Thr Thr Lys Leu Asn Ala Ile Arg Glu Glu Thr Arg Pro Ser  
 210 215 220

Lys Gln Phe Ala Val Pro Ala Lys Pro Trp Pro Ser Ser Asn Thr Arg  
 225 230 235 240

Gln Thr Leu Asp Ser Arg Gln Gly Thr Ala Ala Ser Arg Ala Lys Ala  
 245 250 255

Arg Ser Pro Ser Pro Arg Pro Arg Arg Gln Ser Asn Gly Lys Ala Thr  
 260 265 270

Asp Thr Arg Gly Gly Asn Lys Val Val Asp Glu Leu Lys Pro Lys Gly  
 275 280 285

Ala Ser Ser Ser Gln Ser Gly Ser Ala Ala Ala Ala Thr Ala Lys  
 290 295 300

Arg Met Ala Gly Ser Ser Lys Met Arg Val Ile Pro Ser Arg Tyr Ser  
 305 310 315 320

Leu Thr Pro Gly Ala Ser Leu Gly Ser Ser Gly Ala Gln Glu Arg Arg  
 325 330 335

Arg Lys Gln Ser Leu Pro Gly Ser Ser Gly Asp Ala Asn Gln Asn Glu  
 340 345 350

Glu Ile Arg Ala Lys Val Ile Glu Pro Ser Asn Asp Pro Leu Ser Pro  
 355 360 365

Gln Thr Ile Ser Lys Val Ala Glu Met Leu Pro Lys Ile Arg Thr Met  
 370 375 380

Pro Pro Pro Asp Glu Ser Pro Arg Asp Ser Gly Cys Ala Lys Arg Val  
 385 390 395 400

Ala Glu Leu Val Gly Lys Arg Ser Phe Phe Thr Ala Ala Ala Glu Asp  
 405 410 415

Gly Arg Ala Leu Asp Val Glu Ala Pro Glu Ala Val Ala Glu Ala  
 420 425 430

&lt;210&gt; 5

&lt;211&gt; 1860

&lt;212&gt; DNA

&lt;213&gt; Medicago trunculata

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; seedy1 coding sequence

&lt;400&gt; 5

aaaaacgtta	aggactaaaa	atataataaa	atttaagtag	ggattcataa	tggaagcacc	60
cctatttaca	gggatcttaa	atataattaa	ccctaattatt	tatgacagaa	acccttttga	120
aatcacatcg	gagcgtgtat	gagtagccgt	ttcacatcca	acggccagta	agagcgtaac	180
tttattttct	ccctcttcaa	tctccaacgg	tcacataatc	tcttccaaat	acaaataatt	240
ccctctttca	acctcactct	tcattttctt	aacccaaacc	caaaaaacta	atcagattct	300
tcttaaattct	tgaaaccttt	ctcccaaaag	cacttaaata	aaaaagcact	taaccatgaa	360

## CD105PCT.ST25.txt

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taacacaaac aacaacaaca ttcttcttca ttccacacag gttcaagtgt ggaacaacgc 420
agcattcgat ggtgaagatt tcgccatgaa ttcatcttct gattccatca aagagaatct 480
aaacccatcc gcattcaaca ttgttccttc ttcaaacaaa agaactattg atgatgaaat 540
tgcggaaatt gaaagtgaat ttaagcgatt aacttcgaag ctggaattgc ttcgtgttga 600
aaaagctgaa agaaaaatcg cttctgaaaa gcgtgttagt ggaattggta ctggaagaat 660
agtagcagcg aagtttatgg aaccgaagaa aaacgttaca ccgaaacgaa acggtgtcgt 720
tttcaaggag gagacaccga aacgaaacgg tgtcgtttcg gatacgccga aatctagggt 780
taattggaga agagggatga gtttaggtcc gatggagatt gccgggaaag tgatggcacc 840
gccggcgatg acgattactc cggcgacggg gaatcggagg aagtcttggt tctggaaacc 900
gcaggaaagt tgtgaagtaa tgccgtcggg gattactccg gcgacggtga ataggaggaa 960
atcttgtttt ttgaaacctc aagaaaagttg tgaagaaaat cgaagaaaaa cgatttgcaa 1020
accgaatttg aatttgaatt caaattcagt taattctgcg gttggatcga ttaagcgtgt 1080
gaagaagaaa gatgaagaaa ttgctcaggt tcaaccgaag aagctgtttg aaggtgaaaa 1140
atcagtgaag aaatcgttga aacaaggtag aattgttgca agccggtata attccggtgg 1200
tggttggtgg gatgagagga aaagatcgtt ttcggagaat aataaggggt tagggagtga 1260
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tatgttaccg aagatttctga caatgaggtt tggtgatgag agtccatagag attctgggtc 1380
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agatgatgat gatgatgat attatggtga acaagggtaa ttgtggaaat tgggaattgat 1560
ttgtttttgt ggggtttgtt ggaactggct atgttctgct tgattctttt gcattttggt 1620
gtgaaactaa agatgaggtg aaaagtttat gcttgttaaa ttggattggt ttatatgttt 1680
tgaataataa acaacaagca tgtgtcttgc ttaataattg tatattgttt tgtttgtttt 1740
ataatgatat ggatttaatt tgtatacaca atataatata gtatgcattg agagagtttt 1800
tcggttcagta ttcattctga ttttagtggt tatctcattc tagaagattg tattttgttg 1860

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<210> 6
<211> 394
<212> PRT
<213> Medicago trunculata

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<220>
<221> MISC_FEATURE
<223> seedyl protein

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<400> 6
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Gln Val Trp Asn Asn Ala Ala Phe Asp Gly Glu Asp Phe Ala Met Asn
20 25 30
Ser Ser Ser Asp Ser Ile Lys Glu Asn Leu Asn Pro Ser Ala Phe Asn
35 40 45
Ile Val Pro Ser Ser Asn Lys Arg Thr Ile Asp Asp Glu Ile Ala Glu
50 55 60
Ile Glu Ser Glu Ile Lys Arg Leu Thr Ser Lys Leu Glu Leu Leu Arg
65 70 75 80
Val Glu Lys Ala Glu Arg Lys Ile Ala Ser Glu Lys Arg Val Ser Gly
85 90 95
Ile Gly Thr Gly Arg Ile Val Ala Ala Lys Phe Met Glu Pro Lys Lys
100 105 110
Asn Val Thr Pro Lys Arg Asn Gly Val Val Phe Lys Glu Glu Thr Pro
115 120 125

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## CD105PCT.ST25.txt

Lys Arg Asn Gly Val Val Ser Asp Thr Pro Lys Ser Arg Val Asn Trp  
 130 135 140  
 Arg Arg Gly Met Ser Leu Gly Pro Met Glu Ile Ala Gly Lys Val Met  
 145 150 155 160  
 Ala Pro Pro Ala Met Thr Ile Thr Pro Ala Thr Val Asn Arg Arg Lys  
 165 170 175  
 Ser Cys Phe Trp Lys Pro Gln Glu Ser Cys Glu Val Met Pro Ser Gly  
 180 185 190  
 Ile Thr Pro Ala Thr Val Asn Arg Arg Lys Ser Cys Phe Leu Lys Pro  
 195 200 205  
 Gln Glu Ser Cys Glu Glu Asn Arg Arg Lys Thr Ile Cys Lys Pro Asn  
 210 215 220  
 Leu Asn Leu Asn Ser Asn Ser Val Asn Ser Ala Val Gly Ser Ile Lys  
 225 230 235 240  
 Arg Val Lys Lys Lys Asp Glu Glu Ile Ala Gln Val Gln Pro Lys Lys  
 245 250 255  
 Leu Phe Glu Gly Glu Lys Ser Val Lys Lys Ser Leu Lys Gln Gly Arg  
 260 265 270  
 Ile Val Ala Ser Arg Tyr Asn Ser Gly Gly Gly Gly Asp Ala Arg  
 275 280 285  
 Lys Arg Ser Phe Ser Glu Asn Asn Lys Gly Leu Gly Ser Glu Ile Arg  
 290 295 300  
 Ala Lys Lys Arg Trp Glu Ile Pro Ile Glu Glu Val Asp Val Ser Gly  
 305 310 315 320  
 Phe Val Met Leu Pro Lys Ile Ser Thr Met Arg Phe Val Asp Glu Ser  
 325 330 335  
 Pro Arg Asp Ser Gly Ala Val Lys Arg Val Ala Glu Leu Asn Gly Lys  
 340 345 350  
 Arg Ser Tyr Phe Cys Asp Glu Asp Glu Glu Glu Arg Val Met Val Glu  
 355 360 365  
 Glu Glu Gly Gly Ser Val Cys Gln Val Leu Asn Phe Ala Glu Asp Asp  
 370 375 380  
 Asp Asp Asp Asp Asp Tyr Gly Glu Gln Gly  
 385 390

<210> 7  
 <211> 674  
 <212> DNA  
 <213> Saccharum sp.

<220>  
 <221> misc\_feature

## CD105PCT.ST25.txt

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<223> seedy1 coding sequence (partial 5' end)

<220>
<221> misc_feature
<222> (362)..(362)
<223> n can be a, c, g or t

<220>
<221> misc_feature
<222> (372)..(372)
<223> n can be a, c, g or t

<220>
<221> misc_feature
<222> (674)..(674)
<223> n can be a, c, g or t

<400> 7
cgcacccgga gtttcgaaaa accaacctat cgcgcctcag atcacgcgag gacgcgaggg      60
gaagcaggaa tccctccgct cccagccgcc tcctccgctc acccatcgat cgatcggtccg      120
tccgggtccag ggggtctctc ggcggcggtg gcgatggagg aggaccgct catcccgctg      180
gtgcacgtct ggaacaacgc cgccttcgac cagcctcct cctccgcgtg gcacgcccac      240
tccccctgtgc ccgcgagcgc acgtcgcgag gcggaggggg acaaggagaa ccaccgcccc      300
gaccccgacc ccgacgtcga ggcggagatc ggccacatcg aggcggagat cctgcgcctg      360
tntcccgcc tncaccacct tcgcacctcc aagcagtcgg agccgtccaa gcgcggagag      420
gtcgcgcccg cgcccgcggc gaaggcgaaa gcggcgcgcg cggcgcggct gcggacgcgg      480
gggtcagcc tgggcccgcct cgacgtcgcc gctgcgggta accccaaccc gctcaccacc      540
gacaaccagc agcagcagcc gcgtgccgcg caggggtctga agccgatcaa gcaggccacg      600
gcggcgggcg gcaagggcgt aagacttggg ccccttcgac atggtcggcg cgaaccctag      660
ggtccctccg ccn                                     674

<210> 8
<211> 166
<212> PRT
<213> Saccharum sp.

<220>
<221> MISC_FEATURE
<223> seedy1 protein

<220>
<221> MISC_FEATURE
<223> seedy1 protein (partial N term)

<220>
<221> MISC_FEATURE
<222> (70)..(70)
<223> Xaa can be any amino acid

<400> 8
Met Glu Glu Asp Pro Leu Ile Pro Leu Val His Val Trp Asn Asn Ala
1          5          10          15

Ala Phe Asp His Ala Ser Ser Ser Ala Trp His Ala His Ser Pro Val
20          25          30

Pro Ala Ser Ala Arg Arg Glu Ala Glu Gly Asp Lys Glu Asn His Arg
35          40          45

```



## CD105PCT.ST25.txt

Pro Asp Pro Asp Pro Asp Val Glu Ala Glu Ile Gly His Ile Glu Ala  
 50 55 60

Glu Ile Leu Arg Leu Xaa Ser Arg Leu His His Leu Arg Thr Ser Lys  
 65 70 75 80

Gln Ser Glu Pro Ser Lys Arg Gly Glu Val Ala Pro Ala Pro Ala Ala  
 85 90 95

Lys Ala Lys Ala Ala Ala Ala Arg Leu Arg Thr Arg Gly Leu Ser  
 100 105 110

Leu Gly Pro Leu Asp Val Ala Ala Ala Gly Asn Pro Asn Pro Leu Thr  
 115 120 125

Thr Asp Asn Gln Gln Gln Gln Pro Arg Ala Ala Gln Gly Leu Lys Pro  
 130 135 140

Ile Lys Gln Ala Thr Ala Ala Ala Gly Lys Gly Val Arg Leu Gly Pro  
 145 150 155 160

Leu Arg His Gly Arg Arg  
 165

<210> 9  
 <211> 876  
 <212> DNA  
 <213> Zea mays

<220>  
 <221> misc\_feature  
 <223> seedy1 coding sequence (partial 3' end)

<220>  
 <221> misc\_feature  
 <222> (869)..(869)  
 <223> n = a, c, g or t

<400> 9  
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 ccagaccgtg gccatccagc aatgccaggc acccactgga tgccaggcaa ggcaccgcag 120  
 caagcagagc caaggcagag agcgggagca taagccccag cagggttcagg aggcagtcca 180  
 cttccaagc tgccgagaca agagcgggaa atgccaagcc tacagaggcg acgaggggag 240  
 ggagcgaagc ggtcaatcac accagcaatg tagccacgac gaagaggccg gcggggagct 300  
 ccaaggtcag gggtgtcccc agccgctaca gcatccacc tggctcctcc ctagcagctg 360  
 tgacacaagg caaccgatgc aagcagtctc tcccaggatc ggctactgag accagagtaa 420  
 atctcactga gccgccgaac gacgagttgt ctctgaaga acttgccaag gttgcagagc 480  
 tgctcccaag gattaggacc atgccgcctt ctgatgagag cccgcgtgac tcgggatgtg 540  
 ccaagcgtgt tgctgatttg gtcgggaagc gatccttctt cactgctgca ggggacgatg 600  
 gcaatctcgt tacgccctac caggcacggg tggttgaact tgaatcaccg gaggcagcag 660  
 cagaagaagc agaagcttga gaagtttgtc tttgatcaat tccgaagtgg cttgcatctg 720  
 ggcgtggcct ctttttgcag tgtgtgtctac tacatagtct actgtttacat tcatatcata 780  
 tcacatttcc tattttttcc cccttgagac attgcttagt acttttgtgt tgccttgtga 840  
 aaagagagtg gaaggttcat ctgctgatnc cttgtt 876

<210> 10  
 <211> 224  
 <212> PRT  
 <213> Zea mays

CD105PCT.ST25.txt

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<220>
<221> MISC_FEATURE
<223> seedy1 protein (partial C term)

<400> 10
Thr Arg Pro Ala Val Arg Glu Glu Glu Gly Gln Arg Ser Lys Glu His
1          5          10          15

Ala Val Pro Ala Arg Pro Trp Pro Ser Ser Asn Ala Arg His Pro Leu
          20          25          30

Asp Ala Arg Gln Gly Thr Ala Ala Ser Arg Ala Lys Ala Arg Ser Gly
          35          40          45

Ser Ile Ser Pro Ser Arg Phe Arg Arg Gln Ser Thr Ser Lys Ala Ala
          50          55          60

Glu Thr Arg Ala Gly Asn Ala Lys Pro Thr Glu Ala Thr Arg Gly Gly
65          70          75          80

Ser Glu Ala Val Asn His Thr Ser Asn Val Ala Thr Thr Lys Arg Pro
          85          90          95

Ala Gly Ser Ser Lys Val Arg Val Val Pro Ser Arg Tyr Ser Ile Pro
          100         105         110

Pro Gly Ser Ser Leu Ala Ala Val Thr Gln Gly Asn Arg Cys Lys Gln
          115         120         125

Ser Leu Pro Gly Ser Ala Thr Glu Thr Arg Val Asn Leu Thr Glu Pro
          130         135         140

Pro Asn Asp Glu Leu Ser Pro Glu Glu Leu Ala Lys Val Ala Glu Leu
145         150         155         160

Leu Pro Arg Ile Arg Thr Met Pro Pro Ser Asp Glu Ser Pro Arg Asp
          165         170         175

Ser Gly Cys Ala Lys Arg Val Ala Asp Leu Val Gly Lys Arg Ser Phe
          180         185         190

Phe Thr Ala Ala Gly Asp Asp Gly Asn Leu Val Thr Pro Tyr Gln Ala
          195         200         205

Arg Val Val Glu Leu Glu Ser Pro Glu Ala Ala Ala Glu Glu Ala Glu
          210         215         220

<210> 11
<211> 1257
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> misc_feature
<223> seedy1 coding sequence

<400> 11
atgacatcaa ttgaggcaac agaaacgctt aacgctcctc caaagcttca gatctggaac

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## CD105PCT.ST25.txt

```

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gtttcctctt cgctccaatc ctcagtctcg atcaccgaag ctccgtcagc aaaatccaag 240
accgtgaaga ccaaattccgc cgcagatcgg agtaaaaagc gagatatcga tgcagagatc 300
gaagaagtag agaaggagat cggacgatta tcgacgaaat tggagtcgct ccgattagag 360
aaggcggagc aaaccgcaag aagcattgct atacgtggaa gaatcgttcc ggcgaagttc 420
atggaatcat ctcagaaaca agtgaaattc gacgattcgt gttttacagg atcgaaatca 480
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```

```

<210> 12
<211> 402
<212> PRT
<213> Arabidopsis thaliana

```

```

<220>
<221> MISC_FEATURE
<223> seedyl protein

```

```

<400> 12
Met Thr Ser Ile Glu Ala Thr Glu Thr Leu Asn Ala Pro Pro Lys Leu
1 5 10 15
Gln Ile Trp Asn Asn Ala Ala Phe Asp Asp Gly Asp Ser Gln Ile Thr
20 25 30
Ser Ala Ile Glu Ala Ser Ser Trp Ser His Leu Asn Glu Ser Phe Asp
35 40 45
Ser Asp Cys Ser Lys Glu Asn Gln Phe Pro Ile Ser Val Ser Ser Ser
50 55 60
Leu Gln Ser Ser Val Ser Ile Thr Glu Ala Pro Ser Ala Lys Ser Lys
65 70 75 80
Thr Val Lys Thr Lys Ser Ala Ala Asp Arg Ser Lys Lys Arg Asp Ile
85 90 95
Asp Ala Glu Ile Glu Glu Val Glu Lys Glu Ile Gly Arg Leu Ser Thr
100 105 110
Lys Leu Glu Ser Leu Arg Leu Glu Lys Ala Glu Gln Thr Ala Arg Ser
115 120 125
Ile Ala Ile Arg Gly Arg Ile Val Pro Ala Lys Phe Met Glu Ser Ser
130 135 140
Gln Lys Gln Val Lys Phe Asp Asp Ser Cys Phe Thr Gly Ser Lys Ser

```

## CD105PCT.ST25.txt

```

145                150                155                160
Arg Ala Thr Arg Arg Gly Val Ser Leu Gly Pro Ala Glu Ile Phe Asn
                165                170                175
Ser Ala Lys Lys Ser Glu Thr Val Thr Pro Leu Gln Ser Ala Gln Asn
                180                185                190
Arg Arg Lys Ser Cys Phe Phe Lys Leu Pro Gly Ile Glu Glu Gly Gln
                195                200                205
Val Thr Thr Arg Gly Lys Gly Arg Thr Ser Leu Ser Leu Ser Pro Arg
                210                215                220
Ser Arg Lys Ala Lys Met Thr Ala Ala Gln Lys Gln Ala Ala Thr Thr
                225                230                235                240
Val Gly Ser Lys Arg Ala Val Lys Lys Glu Glu Gly Val Leu Leu Thr
                245                250                255
Ile Gln Pro Lys Arg Leu Phe Lys Glu Asp Glu Lys Asn Val Ser Leu
                260                265                270
Arg Lys Pro Leu Lys Pro Gly Arg Val Val Ala Ser Arg Tyr Ser Gln
                275                280                285
Met Gly Lys Thr Gln Thr Gly Glu Lys Asp Val Arg Lys Arg Ser Leu
                290                295                300
Pro Glu Asp Glu Glu Lys Glu Asn His Lys Arg Ser Glu Lys Arg Arg
                305                310                315                320
Ala Ser Asp Glu Ser Asn Lys Ser Glu Gly Arg Val Lys Lys Arg Trp
                325                330                335
Glu Ile Pro Ser Glu Val Asp Leu Tyr Ser Ser Gly Glu Asn Gly Asp
                340                345                350
Glu Ser Pro Ile Val Lys Glu Leu Pro Lys Ile Arg Thr Leu Arg Arg
                355                360                365
Val Gly Gly Ser Pro Arg Asp Ser Gly Ala Ala Lys Arg Val Ala Glu
                370                375                380
Leu Gln Ala Lys Asp Arg Asn Phe Thr Phe Cys Gln Leu Leu Lys Phe
                385                390                395                400
Glu Glu

```

&lt;210&gt; 13

&lt;211&gt; 3074

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Sequence of the [PRO0090 - CDS0689 - terminator] expression cassette

## CD105PCT.ST25.txt

&lt;400&gt; 13

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ttattgtaaa gttctacaaa gctaatttaa aagttattgc attaacttat ttcattattac 180
aaacaagagt gtcaatggaa caatgaaaac catatgacat actataattt tgtttttatt 240
attgaaatta tataattcaa agagaataaa tccacatagc cgtaaagttc tacatgtggt 300
gcattacca aatataatata gttacaaaa catgacaagc ttagtttgaa aaattgcaat 360
ccttatcaca ttgacacata aagtgagtga tgagtcataa tattattttc tttgttacc 420
atcatgtata tatgatagcc acaaagttac tttgatgatg atatcaaaga acatttttag 480
gtgcacctaa cagaatatcc aaataatatg actacttag atcataatag agcatcaagt 540
aaaactaaca ctctaaagca accgatggga aagcatctat aaatagacaa gcacaatgaa 600
aatcctcatc atccttcacc acaattcaaa tattatagtt gaagcatagt agtaatttaa 660
atcaactagg gatatacaaa gtttgtacaa aaaagcaggc tggtagcggg cgggaattcc 720
cgggatatcg tcgacccacg cgtccgctga cgcgtgggtt ccactacatc aagacatcta 780
ctacactcat cttttttgca cttattgggt gtaaattttt gaaaccaggt tgagaaaaat 840
gagtgtgtta caataccag aagggattga cccagcagat gttagatata ggaacaatgc 900
agcatttgat aatggagatt ctgaagattt gtcttcgctg aaacgttctt ggtctcctct 960
gaaacccctt tcggttaggc catcagattc ctttgaatct gatttgtcaa gtaaggaaaa 1020
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acttaaccct aatggggctc tggaaaattc aagactcaag ccgaacaagc ccaattccaa 1140
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aaaaaacaca gtaattaca agcacaacaa atggtacaag aaaaacagtt ttccaatgc 3060
cataatactc gaac 3074

```

&lt;210&gt; 14

&lt;211&gt; 668

&lt;212&gt; DNA

<213> *Oryza sativa*

## CD105PCT.ST25.txt

```

<220>
<221> misc_feature
<223> prolamin RP6 promoter sequence

<400> 14
ccttctacat cggcttaggt gtagcaacac gactttatta ttattattat tattattatt      60
attatttttac aaaaatataa aatagatcag tccctcacca caagtagagc aagttggtga      120
gttattgtaa agttctacaa agctaattta aaagttattg cattaactta ttcatatta      180
caaacaagag tgtcaatgga acaatgaaaa ccatatgaca tactataatt ttgtttttat      240
tattgaaatt atataattca aagagaataa atccacatag ccgtaaagtt ctacatgtgg      300
tgcattacca aaatatatat agcttacaaa acatgacaag cttagtttga aaaattgcaa      360
tccttatcac attgacacat aaagtgagtg atgagtcata atattatfff tcttgctacc      420
catcatgtat atatgatagc cacaaggtta ctttgatgat gatatcaaag aacattttta      480
ggtgcaccta acagaatatc caaataatat gactcactta gatcataata gagcatcaag      540
taaaactaac actctaaagc aaccgatggg aaagcatcta taaatagaca agcacaatga      600
aaatcctcat catccttcac cacaattcaa atattatagt tgaagcatag tagtagaatc      660
caacaaca

<210> 15
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> Motif 1 CORE SEQUENCE

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> Xaa can be any amino acid

<220>
<221> MISC_FEATURE
<222> (5)..(6)
<223> Xaa can be any amino acid

<400> 15
Trp Xaa Asn Ala Xaa Xaa Asp
1          5

<210> 16
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> Motif 2 CORE SEQUENCE

<220>
<221> MISC_FEATURE
<222> (4)..(5)
<223> Xaa can be any amino acid

<400> 16
Lys Glu Asn Xaa Xaa Pro
1          5

<210> 17
<211> 15

```

CD105PCT.ST25.txt

<212> PRT  
<213> Artificial sequence

<220>  
<223> Motif 3 (coiled coil) CORE SEQUENCE

<220>  
<221> MISC\_FEATURE  
<222> (2)..(2)  
<223> Xaa can be a stretch of 1 to 6 amino acids

<220>  
<221> MISC\_FEATURE  
<222> (4)..(5)  
<223> Xaa can be any amino acid

<220>  
<221> MISC\_FEATURE  
<222> (8)..(10)  
<223> Xaa can be any amino acid

<220>  
<221> MISC\_FEATURE  
<222> (12)..(13)  
<223> Xaa can be any amino acid

<400> 17  
Glu Xaa Glu Xaa Xaa Arg Leu Xaa Xaa Xaa Leu Xaa Xaa Leu Arg  
1 5 10 15

<210> 18  
<211> 15  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Motif 4 CORE SEQUENCE

<220>  
<221> MISC\_FEATURE  
<222> (3)..(3)  
<223> Xaa can be any amino acid

<220>  
<221> MISC\_FEATURE  
<222> (5)..(5)  
<223> Xaa can be a stretch of 1 to 10 amino acids

<220>  
<221> MISC\_FEATURE  
<222> (10)..(11)  
<223> Xaa can be any amino acid

<220>  
<221> MISC\_FEATURE  
<222> (14)..(14)  
<223> Xaa can be a stretch of 1 to 6 amino acids

<400> 18

CD105PCT.ST25.txt

Leu	Pro	Xaa	Ile	Xaa	Arg	Asp	Ser	Gly	Xaa	Xaa	Lys	Arg	Xaa	Lys
1				5					10					15